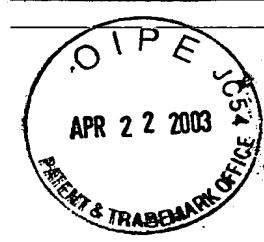


Fig. 1



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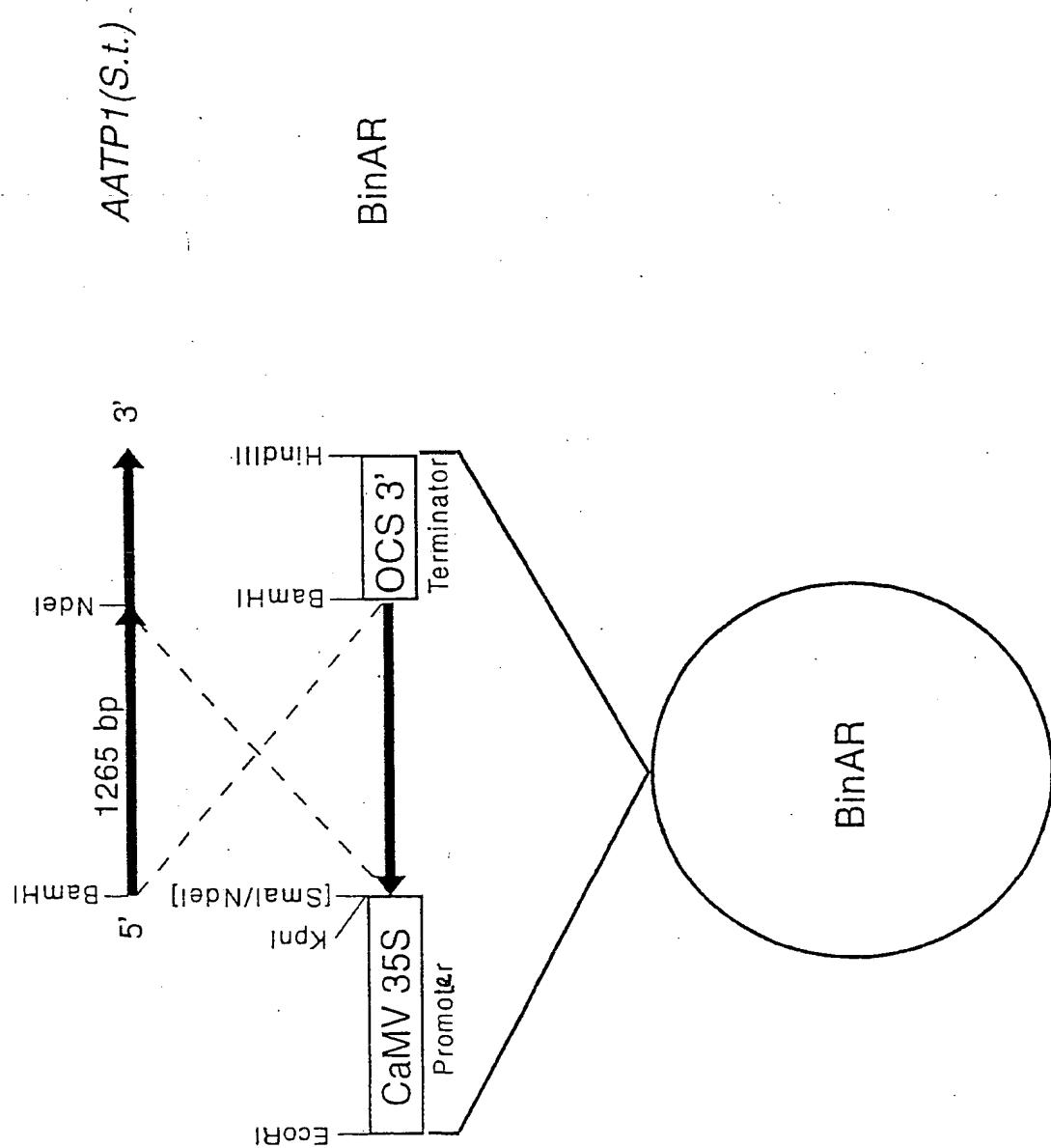


Fig. 2

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DC Alignment:
1 AATP1_A.T.
2 AATP2_A.t
3 TLC

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10 20 30 40 50 60
1 MEAVIQTRGLLSLPTKPIGVRSQLQPSHGLKQRLFAAKPRNLHGCLYPLTGRNFKPLSQ 60
2 MEGLIQTRGILSLPASHR-SEKVLQPSHGLKQRLFTTN--LPALSLSLMVTRNFKPKFSK 56
3 -----MS-----TSK-----SENY--LS- 11

70 80 90 100 110 120
1 PCMGFRFPTKREAPSSYARRRGWCRRSCLRRSDSAAVVASRKIFGVEVATLKKIPLGL 120
2 SHLGFRFPTRREAEDSLARRKLRRRKCVDGDTAAMAVSPKIFGVEVTLKKIVPLGL 116
3 -----EL-----RKIWP-----IEQYENKKFLPLAF 33

130 140 150 160 170 180
1 MFFCILFNYTILRDTKDVLVVTAKGSSAEIIPFLKTWVNLPMMAIGFMLLYTKLSNVLSKK 180
2 MFFCILFNYTILRDTKDVLVVTAKGSSAEIIPFLKTWVNVPMMAIGFMLLYTKLSNVLSKK 176
3 MMFCILLNYSTLRSIKDGFVVTIDG-T-ESISFLKTYIVLPSAVIAMIYVKLCDILKQE 91

190 200 210 220 230 240
1 ALFYTVIVPFIYFGFGFVMYPLSNYIHPEALADKLLTLGPRFMGPIALRIWSFCLF 240
2 ALFYTVIVPFIYFGAFGFVMYPRSNLIQPEALADKLLATLGPRFMGPLAIMRIWSFCLF 236
3 NVFYVITSFFLGYFALFAFVLYPYPDLVHPDHKTIESLSLAYPNFKWFIKIVGKWSFASF 151

250 260 270 280 290 300
1 YVMAELWGSVVSVLFWFANQITVDEAKKFYPLFGIGANVALIFSGRTVKYFSNLRKN 300
2 YVMAELWGSVVSVLFWFANQITVDEAKKFYPLFGLGANVALIFSGRTVKYFSNMRKN 296
3 YTIAELWGTMMLSLLFWQFANQITKIAEAKRFYSMFGLLANLALPVTSVVIGYFLHEKTQ 211

310 320 330 340 350 360
1 LGPGVDGSFV--ESHDEHCGGNTRICLISIGGSNRYV--P-L--PTRSKNKEPKMGT 352
2 LGPGVDGWAWSLKAMMSIVVMGLAICFLYWWVNRYV--P-L--PTRSKKKVKPKQMG 350
3 I-VAEHLKFV--PLFVIMITSSFLIILTYRWMNKVLTDPRLYDPAVKEKKTAKLSF 267

370 380 390 400 410 420
1 MESLKFLVSSPYIRDLATLTVVAYGISINLVEVTWKSCLKAQFPSPNEYSAMGAFSTCTG 412
2 MESLKFLVSSPYIRDLATLTVVAYGISINLVEVTWKSCLKSQFPSPNEYSAMGDFSTCTG 410
3 IESLKMIIFTSKYVGYTALLIAYGVSVNLVEGVWVKSKVKELYPTKEAYTIYMGQFQFYQG 327

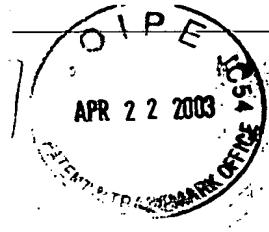
430 440 450 460 470 480
1 VATFTMMLLSQYVFNKYWGVAAKITPTVLLTGVAFFSLILFGGPFA-PLVAKLGMTPL 471
2 LATFTMMLLSQYVFKKYWGVAAKITPTVLLTGVAFFSLILFGGPFA-PLVAKLGMTPL 469
3 WVAIAFMLIGSNILRKVSWLTAAMITPLMMFITGAFFSFIFDSVIAMNLTGILASSPL 387

490 500 510 520 530 540
1 LAAVYVGALQNFSK-SAKYSLFDPCKEAMA YIPLDEDTKVKGKAAIDVVCNPLGKSGGAL 530
2 LAAVYVVPPEVSSARVQVQHSSTPSAMQECLYPLDEVSKVKAKLQL-MWSATIGKSGGAL 528
3 TLAVMIGMIQNVLSK-GVKYSLFDATKNMAYIPLDKDLRVKGQAAVEVIGGLGKSGGAI 446

550 560 570 580 590 600
1 IQQ-FMIL--SFGSLANSTPYLGMILLVIVTAWAAKSLEGQFNSLRLKSLRRKWREL 587
2 IQQ-FMIL--TFSGLANSTPYLGVILLGIVTAWAAKSLEGPV----- 569
3 IQSTFFILFPVFGFI-EATPYFASIFFIIVLWIFAVKGLNKEYQVL-VNKNEK----- 498

1 HR 589
2 -- 569
3 -- 498

Fig. 3



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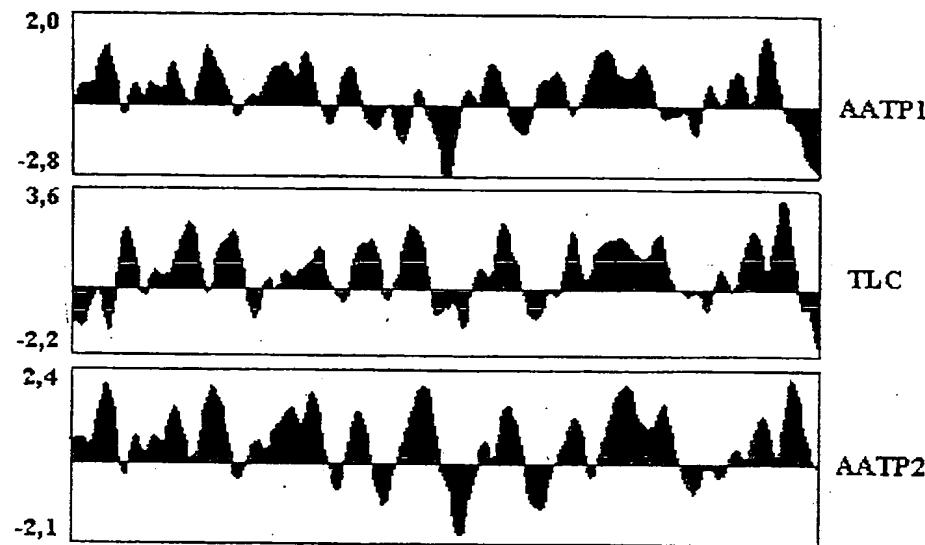
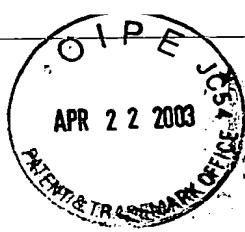


Fig. 4



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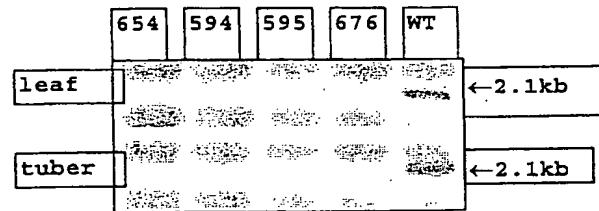


Fig. 5

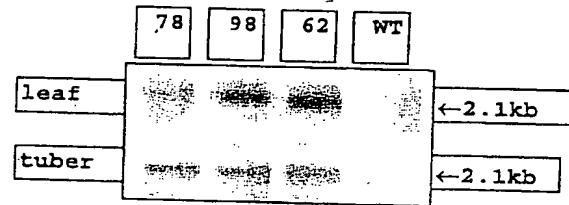


Fig. 6

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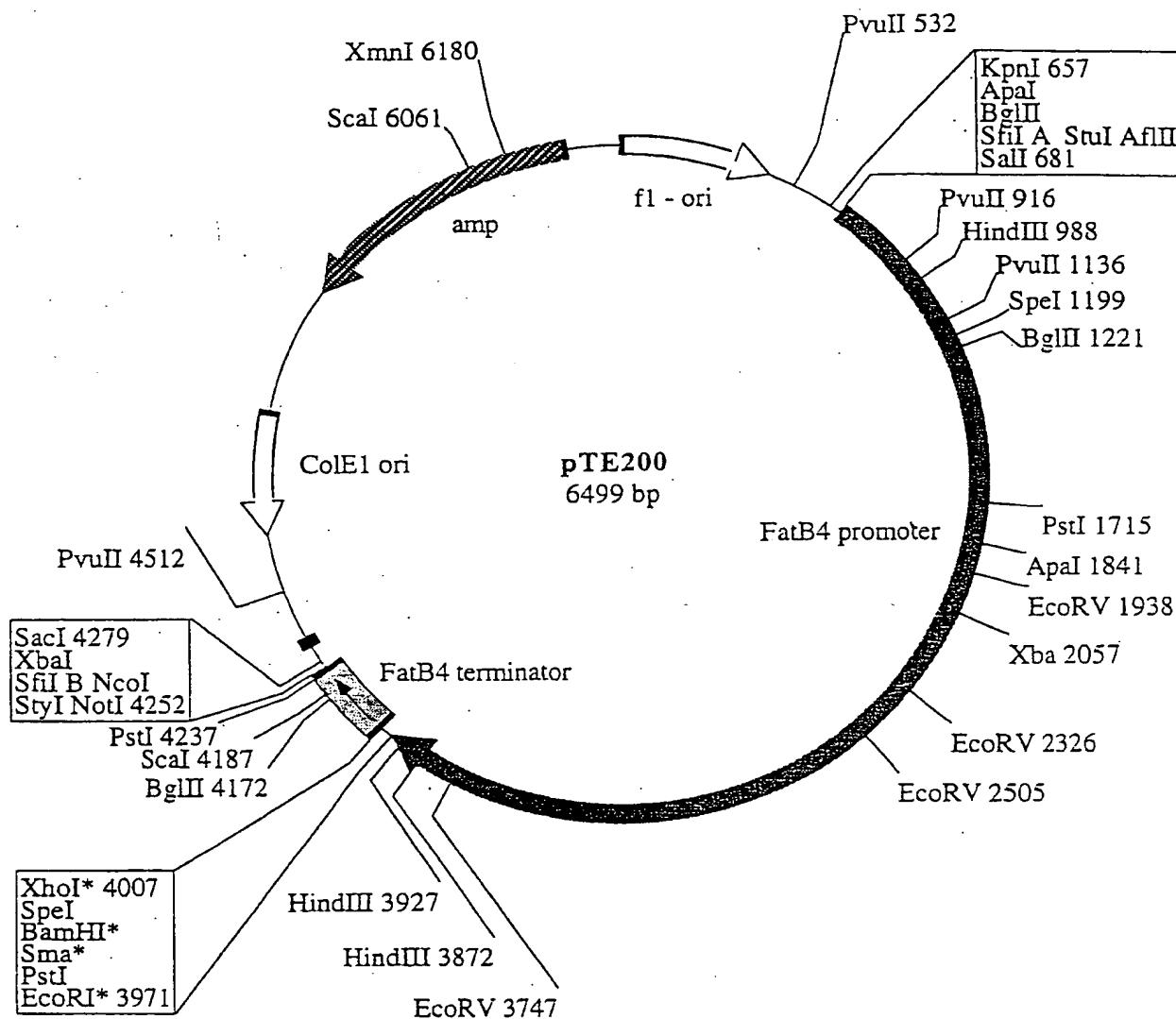


Fig. 7



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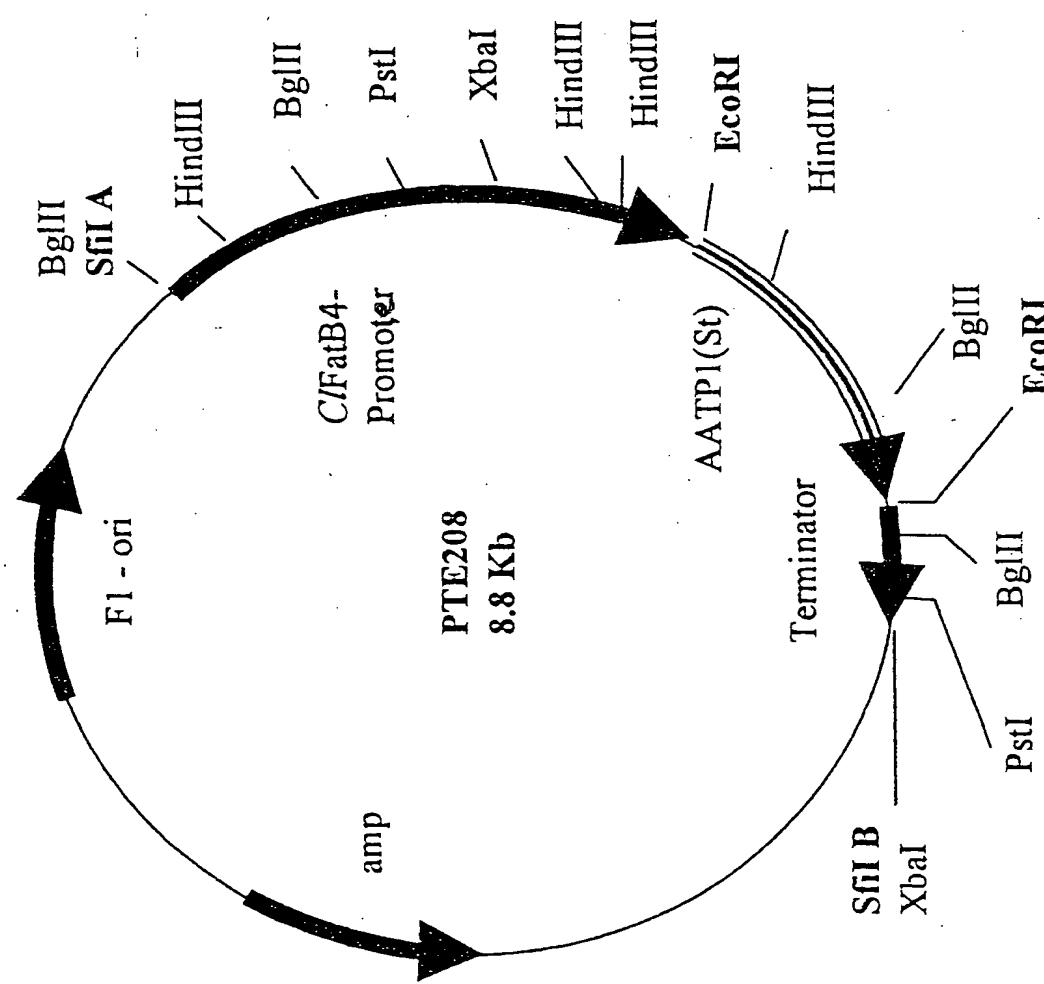


Fig. 8



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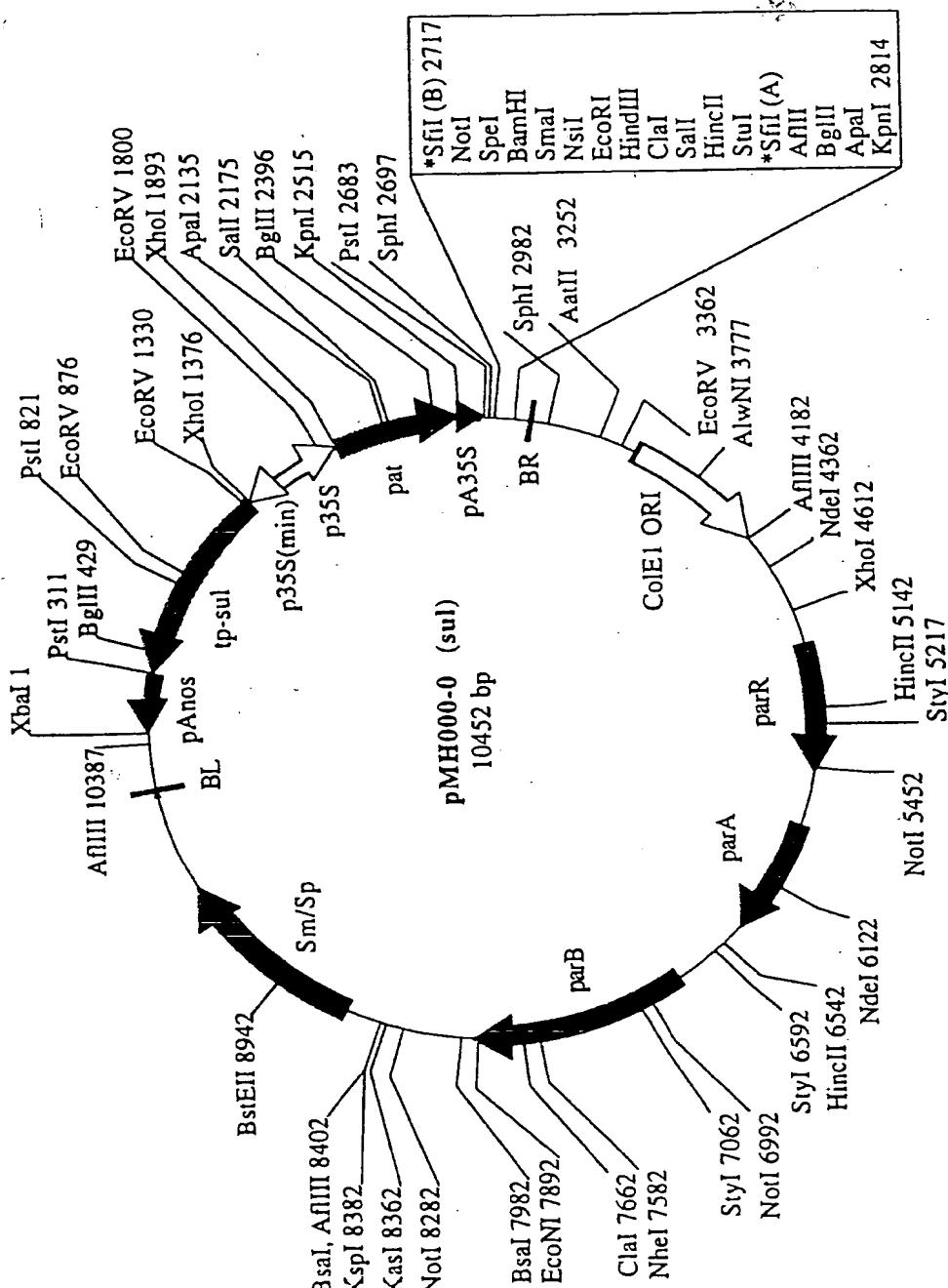


Fig. 9